

GenCore version 4.5
 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 25, 2000, 03:51:15 ; Search time 853.82 Seconds
 (without alignments) 3410.674 Million cell updates/sec

Title: US-09-373-230-1
 Perfect score: 471
 Sequence: 1 AACCTTGGCCGACTTACTG.....TCACTACTACATCAAAGT 471
 Scoring table: IDENTITY_NUC
 Gpop 10.0 , gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*

1: qb.est1:*

2: qb.est2:*

3: qb.est3:*

4: qb.est4:*

5: qb.est5:*

6: qb.est6:*

7: qb.est7:*

8: qb.est8:*

9: qb.est9:*

10: qb.est10:*

11: qb.est11:*

12: qb.est12:*

13: qb.est13:*

14: qb.est14:*

15: qb.est15:*

16: qb.est16:*

17: qb.est17:*

18: qb.est18:*

19: qb.est19:*

20: qb.est20:*

21: qb.est21:*

22: qb.est22:*

23: qb.est23:*

24: qb.est24:*

25: qb.est25:*

26: qb.est26:*

27: qb.est27:*

28: qb.est28:*

29: qb.est29:*

30: qb.est30:*

31: qb.est31:*

32: qb.est32:*

33: qb.est33:*

34: qb.est34:*

35: qb.est35:*

36: qb.est36:*

37: qb.est37:*

38: qb.est38:*

39: qb.est39:*

40: qb.est40:*

41: em.estiba:*

42: em.estfun:*

43: em.esthml:*

44: em.esthun2:*

45: em.esthun3:*

46: em.esthun4:*

47: em.esthun5:*

48: em.esthun6:*

49: em.esthun7:*

50: em.esthun8:*

51: em.esthun9:*

52: em.esthun10:*

53: em.esthun11:*

54: em.esthun12:*

55: em.esthun13:*

56: em.esthun14:*

57: em.esthun20:*

58: em.esthun16:*

59: em.esthun17:*

60: em.esthun18:*

61: em.esthun19:*

62: em.esthun21:*

63: em.estin1:*

64: em.estin2:*

65: em.estin3:*

66: em.estin4:*

67: em.eston:*

68: em.estov1:*

69: em.estov2:*

70: em.estp1:*

71: em.estp12:*

72: em.estp13:*

73: em.estp14:*

74: em.estp15:*

75: em.estrol1:*

76: em.estrol2:*

77: em.estrol3:*

78: em.estrol4:*

79: em.estrol5:*

80: em.estrol6:*

81: em.estrol7:*

82: em.estrol8:*

83: em.estrol9:*

84: em.estrol10:*

85: em.estrol11:*

86: em.estrol12:*

87: em.estrol13:*

88: qb.gss1:*

89: qb.gss2:*

90: qb.gss3:*

91: qb.gss4:*

92: em.gss1:*

93: em.gss2:*

94: em.gss3:*

95: em.gss4:*

96: qb.gss5:*

97: qb.gss6:*

98: qb.gss7:*

99: qb.gss8:*

100: qb.gss9:*

101: em.gss5:*

102: em.gss6:*

103: em.gss7:*

104: em.gss8:*

105: em.gss9:*

106: em.gss10:*

107: em.gss11:*

108: qb.gss10:*

109: qb.gss11:*

110: em.gss12:*

111: qb.gss12:*

112: qb.gss13:*

113: qb.gss14:*

114: qb.gss15:*

115: qb.gss16:*

116: qb.gss17:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	465.8	98.9	603 7	AA930362 vs59ff07_r
C 2	400.6	85.1	645 7	AA892285 EST196088
C 3	365.6	77.6	512 8	AW125102 UT-M-BH2.
C 4	337.6	71.7	474 8	AT121020 ut69cc02_r
C 5	308.6	65.5	434 2	AA237376 mx29g01_r
C 6	274.8	58.2	469 10	AI63005 vB89905_x
C 7	260.8	55.4	423 23	AW558748 L0299E02_r
C 8	239.8	50.9	443 19	AV597984 AV597984
C 9	208.4	44.2	357 19	AW049334 UT-M-BH1-
C 10	207.4	44.0	369 9	AI176343 EST219926
C 11	197.4	41.9	342 13	AT835755 UT-M-A10-
C 12	191.6	40.7	335 15	AV066410 AV066410
C 13	173.4	36.8	289 2	AA245600 mx0Da01_r
C 14	166.8	35.4	505 8	AI106315 ut69cc02_r
C 15	155.6	33.0	574 19	AV597985 AV597985
C 16	153.8	32.7	354 12	AV072353 AV072353
C 17	153.8	32.7	354 12	AT1642457 VV80b10_x
C 18	153.4	32.6	292 15	AV063007 AV063007
C 19	151.6	32.2	287 15	AV065008 AV065008
C 20	148.4	31.5	276 15	AV078115 AV078115
C 21	148.4	31.4	285 15	AV032583 AV032583
C 22	144.4	30.6	306 15	AV069911 AV069911
C 23	142.4	30.2	300 16	AV169683 AV169683
C 24	139.4	29.6	300 17	AV239413 AV239413
C 25	138.4	29.4	294 15	AV067717 AV067717
C 26	138.4	29.3	299 15	AV007682 AV007682
C 27	135.6	28.8	293 15	AV076434 AV076434
C 28	130.4	27.7	279 15	AV087765 AV087765
C 29	124.8	26.5	281 15	AV002592 AV002592
C 30	124.8	26.5	259 15	AV071444 AV071444
C 31	117.2	24.9	259 15	AW338525 xx80b03_x
C 32	114.2	24.9	254 20	AW151778
C 33	92.9	19.5	513 20	AW180476 t114b05_x
C 34	78.7	16.6	655 96	AQ377384 R0C11-16
C 35	63.8	13.5	325 20	AW142292 EST192351
C 36	57.2	12.1	188 18	AV077488 AV077488
C 37	56.6	12.0	468 8	AI120421 qc38911_x
C 38	54.2	11.5	196 18	AV338761 AV328761
C 39	49.6	10.5	309 8	N83242 K4622F R0ma
C 40	47.6	10.1	438 9	AI247015 qx52cl0_x
C 41	42.8	9.1	188 15	AV069285 AV069285
C 42	39.6	8.4	413 99	AQ592903 HS 5453_A
C 43	37.6	8.0	442 1	AI128391 zn85bb03_s
C 44	37.6	8.0	1101 121	CNS0039G
C 45	37.4	7.9	751 23	AW657654 NF011G05P1

ALIGNMENTS

RESULT 2
LOCUS AB892285 /c
DEFINITION EST:196088 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
ACCESSION RK1NO60 3' end, mRNA sequence.
VERSION AB892285.1
KEYWORDS EST
SOURCE Rattus sp.
ORGANISM Rattus
REFERENCE Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Genes Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
ATCC The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301) 838-3529
Fax: (301) 838-0208
Email: nhl@tigr.org

FEATURES source
/organism="Rattus sp."
/db_xref="ATCC (inhost):2017880"
/clone="RK1NO60"
/clone_id="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pRT73pac; Site: 1; ECORI; Site: 2; NotI"; M1-21."
BASE COUNT 177 a 126 c 123 g 220 t
ORIGIN

Query Match 85.1%; Score 400.6; DB 7; Length 646;
Best Local Similarity 91.8%; Prc. No. 4.4e-98;
Matches 434; Conservative 1; Mismatches 35; Indels 3; Gaps 1;

QY 2 ACTTGCGCGACTCTACTGTACAGACCGCACTAATCGGAATAAAGGCCAAAGTGTCT 61
Db 579 ACTTGCGAGCTACTGACTGACAACTGCGAGATAATGCCAAAGTGTCT 520
QY 62 TCGTGTGACAAAGC -- CAGCTGTGCTGAGGTATGACGATGATGTCAAGTCCA 118
Db 519 TCGTGTGACAAAGCAGACCGAGCTGATAATGACAAAGCAGTGAGGAGGTGG 178
QY 119 GNGAACCCGAGCAGCAGCTGATAATGACAAAGCAGTGAGGAGGTGG 400
Db 459 AGCAATCCCGAGCAGCAGCTGATAATGACAAAGCAGTGAGGAGGTGG 400
QY 179 CTGTCACCCCTCTGTGAGGATACTAAAYGCTACCTCTCCCTGAAAGAACAGTCA 238

RESULT 2
LOCUS AB892285
DEFINITION EST:196088 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
ACCESSION RK1NO60 3' end, mRNA sequence.
VERSION AB892285.1
KEYWORDS EST
SOURCE Rattus
ORGANISM Rattus
REFERENCE Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Genes Index
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
ATCC The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301) 838-3529
Fax: (301) 838-0208
Email: nhl@tigr.org

FEATURES source
/organism="Rattus sp."
/db_xref="ATCC (inhost):2017880"
/clone="RK1NO60"
/clone_id="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pRT73pac; Site: 1; ECORI; Site: 2; NotI"; M1-21."
BASE COUNT 177 a 126 c 123 g 220 t
ORIGIN

Query Match 85.1%; Score 400.6; DB 7; Length 646;
Best Local Similarity 91.8%; Prc. No. 4.4e-98;
Matches 434; Conservative 1; Mismatches 35; Indels 3; Gaps 1;

QY 2 ACTTGCGCGACTCTACTGTACAGACCGCACTAATCGGAATAAAGGCCAAAGTGTCT 61
Db 579 ACTTGCGAGCTACTGACTGACAACTGCGAGATAATGCCAAAGTGTCT 520
QY 62 TCGTGTGACAAAGC -- CAGCTGTGCTGAGGTATGACGATGATGTCAAGTCCA 118
Db 519 TCGTGTGACAAAGCAGACCGAGCTGATAATGACAAAGCAGTGAGGAGGTGG 178
QY 119 GNGAACCCGAGCAGCAGCTGATAATGACAAAGCAGTGAGGAGGTGG 400
Db 459 AGCAATCCCGAGCAGCAGCTGATAATGACAAAGCAGTGAGGAGGTGG 400
QY 179 CTGTCACCCCTCTGTGAGGATACTAAAYGCTACCTCTCCCTGAAAGAACAGTCA 238

RESULT 3
LOCUS AM125102/c
DEFINITION AM125102 512 bp mRNA EST 22-OCT-1999
ACCESSION UI-M-BH2.1-apx-g-10-0-01_3' mRNA sequence.
VERSION AM125102.1
KEYWORDS EST
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 435 1706
Fax: 301 443 9890
Email: mbs@nmail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bona fide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized basal ganglia library. CDNA Library Preparation: M.B. Soares lab. Clone distribution: NIH BMAP CDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP CDNA clones, this record will be updated accordingly when that means is determined. The following repetitive elements were found in this cDNA sequence: 17-81->MSTB14TR/MaLR
Seq primer: M13 Forward
POLA-Yes
FEATURES source
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-BH2.1-apx-g-10-0-01_3'"
/clone_id="NIH_BMAP_M_S3.1"
/dev_stage="27-32 days"
/lab_host="BHLB (Life Technologies)"
/note="vector: pRT73Pac (Pharmacia) with a modified polylinker; Site: 1: Not I; Site: 2: Eco RI; The NIH_BMAP_M_S3.1 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse

AUTHORS	JOURNAL
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacy, M., Lein, J., Morris, M., Schellenbach, S., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theiling, B., Willey, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.	The WashU HHMI Mouse EST Project Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu
BASE COUNT	135
ORIGIN	a
Query Match	77.6%; Score 365; DB 20; Length 512;
Best Local Similarity	99.7%; Pred. No. 1.2e-88; Mismatches 365; Conservative 1; Indels 0; Gaps 0;
Matches	365; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	106 GATCAAGTGGCCAGTCACCCAGACAGCTGATAATACTACAGTACAAAGCAGTGA 165
Db	512 GATCAAAGTGGCCAGTCACCCAGACAGCTGATAATACTACAGTACAAAGCAGTGA 453
QY	166 GTAAAGGAGCTGGCTGTGACCCCTCTGTGAGGATAGTAAAGTCTACCCCTCTGT 225
Db	452 GTAAAGGAGCTGGCTGTGACCCCTCTGTGAGGATAGTAAAGTCTACCCCTCTGT 393
QY	226 AAGAACAGAATGATCTCTGTGAGGAATGATCCACCTGAAATATTGTGATATACAA 285
Db	392 AAGAACAGAATGATCTCTGTGAGGAATGATCCACCTGAAATATTGTGATATACAA 333
QY	286 AGTGATCTCATATTCTTCAGAAGCCTGTTCCAGCACACAGATGGTGTGAACT 345
Db	332 AGTGATCTCATATTCTTCAGAACGTTCCAGCACACAGATGGTGTGAACT 273
BASE COUNT	132
ORIGIN	a
Query Match	71.7%; Score 337.6; DB 8; Length 474;
Best Local Similarity	99.7%; Pred. No. 4.4e-81; Mismatches 337; Conservative 1; Indels 0; Gaps 0;
Matches	337; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	134 GACTGATAATACATGTCACAGACAGCTGAGTGTGAGGACTGGCTGTGACCTCTG 193
Db	474 GACTGATAATACATGTCACAGACAGCTGAGTGTGAGGACTGGCTGTGACCTCTG 415
QY	194 TGAAGGATGTAATAAGTGTACCTCTCTGTAGAGAACAGATCATTCCTTGAGGAA 253
Db	414 TGAAGGATGTAATAAGTGTACCTCTCTGTAGAGAACAGATCATTCCTTGAGGAA 355
QY	254 TGGATCACCCTGAAATAATGAGTATACACAGATGTCTCATATTCTTCAGAACGCT 313
Db	354 TGGATCACCCTGAAATAATGAGTATACACAGATGTCTCATATTCTTCAGAACGCT 295
QY	314 TTCCAGGACACACAGATGGAGTTGAACTCTCACGTATGAGGACACTTCTCTCT 373
Db	294 TTCCAGGACACACAGATGGAGTTGAACTCTCACGTATGAGGACACTTCTCTCT 235
RESULT	4
AT121020/C	
LOCUS	A1121020 474 bp mRNA EST 02-SEP-1998
DEFINITION	ud69c02.x1 Sugano mouse liver mRNA clone
IMAGE	1451138 3' similar to gb:D9949 Mouse mRNA for IGF precursor
POLYPEPTIDE	(MOUSE);, mRNA sequence.
ACCESSION	A121020
VERSION	A1121020.1
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
MARYKOTA, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Scurogathi; Muridae; Murinae; Mus.	

RESULT	5	QY	343	TCTTCAGTGTAAAGACACTTCTGCTGCCAAAGGAGATGATGCTTCAAACTC	402
AA237736		Db	181	TCTTCAGTGTAAAGACACTTCTGCTGCCAAAGGAGATGATGCTTCAAACTC	240
LOCUS	AA237736	QY	403	ATTCGAAAGAAAGATGAAATGGGATAATCTGTAATGTCACACTCTACTA	462
DEFINITION	mx2901.r1 Soares mouse NML MUS musculus cDNA clone IMAGE:681648	Db	241	ATTCGAAAGAAAGATGAAATGGGATAATCTGTAATGTCACACTCTACTA	300
ACCESSION	(MOUSE); mRNA sequence.	QY	463	CATCAAGT 471	
VERSION	AA237736.1	Db	301	CATCAAGT 309	
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 1 (bases 1 to 434)				
AUTHORS	Marr,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Scheibenbogen,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.				
TITLE	The WashU-HMM Mouse EST Project				
JOURNAL	Unpublished (1996)				
COMMENT	Contact: Marra M/WashU				
FEATURES	source				
	Washington-HMM Mouse EST Project				
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108				
	Tel: 314 286 1810				
	Fax: 314 286 1810				
	Email: mouseest@watson.wustl.edu				
	IMAGE Consortium (info@image.llnl.gov) for further information.				
	MGI:21352				
	Putative full length read				
	vector to vector length is 437				
	Seq primer: -28m13 rev2				
	Location/Qualifiers				
	1. -434				
	/organism="Mus musculus"				
	/db_xref="txon:10050"				
	/clone="IMAGB:681648"				
	/clone_lib="Soares mouse NML"				
	/tissue_type="Liver"				
	/lab_host="DH10B"				
	/note="Vector: pT7T3-Pac (Pharmacia) with a modified				
	polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA				
	was primed with a Not I - oligo(dT) primer [5'				
	TGTCACCACTCGAAGGGCGGCGGAGAACCTTCTTCTTCTT 31];				
	double-stranded cDNA was ligated to Eco RI adaptors				
	(Pharmacia), digested with Not I and cloned into the Not I				
	and Eco RI sites of the modified pT7T3 vector. Library				
	constructed and normalized by Bento Soares and M.Fatima				
	Bonaldo."				
BASE COUNT	139 a 79 c 92 g 124 t				
ORIGIN					
Query Match	65.5%; Score 308.6; DB 2; Length 434;				
Best Local Similarity	99.7%; Pred. No. 3e-73;				
Matches	308; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
QY	163 GACTAAGAGGACTGCTGAGCCCTCTGAGGATGATAAATGTCACCTCTCC	222			
Do	1 GAGAAGAGGACTGCTGAGGATGATAAATGTCACCTCTCC	60			
QY	223 TGTAGAAGAGAGATCATTCCTGAGGAATGATCACCCTGAAATATGATGATA	282			
Db	61 TGTAGAAGAGAGATCATTCCTGAGGAATGATCACCCTGAAATATGATGATA	120			
QY	283 CAAAGTGTCTCATATCTCTGAGACACAAAGATGGAGTTGAA	342			
Db	121 CAAAGTGTCTCATATCTCTGAGACACAAAGATGGAGTTGAA	180			
Query Match	58.2%; Score 274; DB 10; Length 469;				
Best Local Similarity	90.7%; Pred. No. 6.9e-64;				

Matches	311;	Conservative	1;	Mismatches	29;	Indels	2;	Gaps	2;
Qy	131	CCAGACTGATAATAACATGTCACAAGCAGTGAAGGACTGCCTGACCCCT	190						
Db	469	CCAGCCTGATTAATCCATGGTCAAAGGCCAGCTGAGTAAGAGGACTGCCTGTC	410						
Qy	191	CTGTGAGGATGTAAGCTCCTCCCTCTGTAAGACAAAGATCATTCCTTGAGG	250						
Db	409	CTGTGAGGATGTAAGCTCCTACCTNCCTGTAAGACAAAGATCATTCCTTGAGG	350						
Qy	251	AAATGGATCCA-CCTGAAATATGATGATAAGTCAAGTGTCTATANTCTTCAGAA	309						
Db	349	AAATGGATCCA-CCTGAAATATGATGATAAGTCAAGTGTCTATANTCTTCAGAA	290						
Qy	310	CGTGTCCAGCACACAGAGATG-GAGTTGATCTCACTCTATGAGGACTCT	368						
Db	289	CGTGTCCAGCACACAGAGATG-GAGTTGATCTCACTCTATGAGGACTCT	230						
RESULT	7								
AW558748/c	AW558748	423 bp	mRNA	EST	02-AUG-2000				
LOCUS	AW558748	131	Mouse Newborn Ovary cDNA Library	Mus musculus	cdna clone				
DEFINITION	LO299E02-3	Mouse Newborn Ovary	cdna Library	Mus musculus	cdna clone				
ACCESSION	AW558748	131							
VERSTON	AW558748.1	1	GI:7204177						
KEYWORDS	EST.								
SOURCE	house mouse.								
ORGANISM	Mus musculus								
Eukaryota;	Metazoa;	Chordata;	Craniata;	Vertebrata;	Euteleostomi;				
Mammalia;	Eutheria;	Rodentia;	Sciurognathi;	Muridae;	Murinae;	Mus.			
1 (bases 1 to 423)									
REFERENCE	Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Negaraja,R., Doi,H., Wood,W.H., III, Becker,K.G. and Ko,M.S.H.								
TITLE	Genome wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray								
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)								
COMMENT	Contact: George J. Kargul								
AUTHORS	Laboratory of Genetics								
National Institute on Aging/National Institutes of Health									
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA									
Email: cdna@gsun.grc.nia.nih.gov									
Plate: L0299	row: E	column: 02							
Seq primer: -21M13 Forward									
High quality sequence stop: 423									
POLYA=Yes.									
FEATURES	Location/Qualifiers								
source	1. .423								
/organism="Mus musculus"									
/strain="C57BL/6J"									
/db_xref="taxon:10090"									
/clone="LO299E02"									
/clone_1.lib="Mouse Newborn Ovary"									
/sex="Female"									
/dev_stage="Newborn Ovary"									
/lab_host="BHLB"									
/note="Vector: PSORT1 (Gibco/BRL Life Technology);									
site_1: SalI; site_2: NotI; total RNAs were extracted from									
7 Newborn Ovary. The double-stranded cDNA was synthesized									
by Gibco's kit with an oligo(dT) primer [NotI									
primer-adapter from GibcoBRL]									
note_1: SalI; site_2: NotI; total RNAs were extracted from									
2.56ug of total RNA. The double-stranded cDNAs were									
treated with T4 DNA Polymerase and purified by									
FEATURES	Location/Qualifiers								
source	1. .443								
/organism="Bos taurus"									
/db_xref="taxon:9913"									

ethanol-precipitation. The cDNAs were ligated to lone-linker LL-Sal3 (include SalI sequence). The cDNAs were purified by phenol/chloroform and separated from free linkers by Centrificon 100. Then, cDNAs were amplified by long-range high fidelity PCR using Takara's Ex Tag polymerase. Then, the cDNAs were purified by phenol/chloroform and by Centrificon 100. The cDNAs were digested with SalI and NotI enzymes. Then the cDNAs were size selected by Gibco's Size Fractionation Column. The cDNAs were cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by chemical method. The library was constructed by Xiaohong Wang and Yulan Piao."

BASE COUNT

116 a

84 c

81 g

142 t

ORIGIN

Query Match

55.4%

Score

260.8

: DB

23;

Length

423;

Best

Local

Similarity

94.9%

: Pred.

No.

2.5e-06;

Mismatches

13;

Indels

1;

Gaps

1;

Matches

279;

Conservative

1;

Mismatches

13;

Indels

1;

Gaps

1;

Best

Local

Similarity

94.9%

: Pred.

No.

2.5e-06;

Mismatches

13;

Indels

1;

Matches

279;

Conservative

1;

Mismatches

13;

Indels

1;

Gaps

1;

Best

Local

Similarity

94.9%

: Pred.

No.

2.5e-06;

Mismatches

13;

Indels

1;

Matches

279;

Conservative

1;

Mismatches

13;

Indels

1;

Gaps

1;

Best

Local

Similarity

94.9%

: Pred.

No.

2.5e-06;

Mismatches

13;

Indels

1;

Matches

279;

Conservative

1;

Mismatches

13;

Indels

1;

Gaps

1;

Best

Local

Similarity

94.9%

: Pred.

No.

2.5e-06;

Mismatches

13;

Indels

1;

Matches

279;

Conservative

1;

Mismatches

13;

Indels

1;

Gaps

1;

Best

Local

Similarity

94.9%

: Pred.

No.

2.5e-06;

Mismatches

13;

Indels

1;

Matches

279;

Conservative

1;

Mismatches

13;

Indels

1;

Gaps

1;

Best

Local

Similarity

94.9%

: Pred.

No.

2.5e-06;

Mismatches

13;

Indels

1;

Matches

279;

Conservative

1;

Mismatches

13;

Indels

1;

Gaps

1;

Best

Local

Similarity

94.9%

: Pred.

No.

2.5e-06;

Mismatches

13;

Indels

1;

Matches

279;

Conservative

1;

Mismatches

13;

Indels

1;

Gaps

1;

Best

Local

Similarity

94.9%

: Pred.

No.

2.5e-06;

Mismatches

13;

Indels

1;

Matches

279;

Conservative

1;

Mismatches

13;

FEATURES	source	COMMENT
BASE COUNT		
ORIGIN		
Query Match	1. . 369	Best Local Similarity 91.3%; Pred. No. 6; 6e-46; Matches 220; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Qy	231 CAAAGATCATTCTTGAGGAATGGATCCACCTGAAATATTGATGATATAACAGTGA 290	
Db	369 CAAATCATCTTCTTGAGGAATGAAATCCCTGAAATATTGATGATATAACAGTGA 310	
Qy	291 TCTCATATCTTCTGAGAACCTGTTCCAGGACACAAAGATGAGCTGAGTTGATCTTCATC 350	
Db	309 TTCAATTCTTCAGAACAGTGTGCCAGGACCCACAAATGGATTGATCTTCCT 250	
Qy	351 GTATGAGGAGCACCTCTGCTGCCAAAGGAGATGATCTTCACACTCATCTGAA 410	
Db	249 GTATGAGGAGCCCTTTAGCTGCTGCCAAAGGAAATGATGCTTCACACTGTTAA 190	
Query Match	1. . 198	Best Local Similarity 99.5%; Pred. No. 3; 2e-43; Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	471 T 471	
Db	129 T 129	
BASE COUNT	98	
ORIGIN	a 68 c 55 g 121 t	
Query Match	1. . 320	Best Local Similarity 99.5%; Pred. No. 3; 2e-43; Matches 198; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	471 T 471	
Db	189 AACGAAGGATGAAATGGGATAATCTGTAATGTTCACTCTTACTAACTTACATCAAG 130	
Query Match	1. . 144	Best Local Similarity 99.5%; Pred. No. 3; 2e-43; Matches 144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	453 CACTACTCATCAAGT 471	
Db	162 CACTACTCATCAAGT 144	
RESULT	11	
AI035755/C	A1835755 342 bp mRNA EST	
LOCUS	AI-M-A10-aan-g-11-0-UI..S1 NIH_BMAP_MBS	
DEFINITION	MUS_musculus cDNA clone	
ACCESSION	AI835755	
VERSION	AI835755.1	
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
REFERENCE	1 (bases 1 to 342)	
AUTHORS	Bonaldo, M.F., Lennon, G. and Soares, M.B.	
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery	
JOURNAL	Genome Res. 6 (9), 791-806 (1996)	
MEDLINE	9704477	
RESULT	12	
AV066410	AV066410 335 bp mRNA EST	
LOCUS	AV066410	
DEFINITION	MUS_musculus small intestine C57BL/6J adult MUS_musculus cDNA clone 2010109E01. mRNA sequence.	
ACCESSION	AV066410	

VERSION	AI046315	EST	08-JUL-1998
LOCUS	AI046315	505 bp	mRNA
DEFINITION	ud69c02.y1 Sugano mouse liver mlia	Mus musculus	cDNA clone
IMAGE	1451138	similar to gb:D49949	Mouse mRNA for IGF precursor
ACCESION	AI046315		polypeptide (MOUSE); mRNA sequence.
TITLE	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
REFERENCE	1 (bases 1 to 505)		
AUTHORS	Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubroque, T., Geisels, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Scheibenbogen, S., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.		
JOURNAL	The WashU-HMMI Mouse EST Project		
COMMENT	Unpublished (1996)		
CONTACT	Marra, M./Mouse EST Project		
WashU-HMMI Mouse EST Project			
Washington University School of Medicine			
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108			
Tel: 314 286 1800			
Fax: 314 286 1810			
Email: mouseest@watson.wustl.edu			
This clone is available royalty-free through LBNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.			
MGIT:924454			
Seq primer: custom primer used			
High quality sequence stop: 385.			
FEATURES	Location/Qualifiers		
source	1..505		
	/organism="Mus musculus"		
	/strain="C57BL"		
	/db_xref="TAXON:10090"		
	/clone="IMAGE:451138"		
	/clone_id="Sugano mouse liver mlia"		
	/sex="female"		
	/dev_stage="adult"		
	/lab_host="DH10B"		
	/note="Organ: liver; Vector: PME18S-FL3; Site_1: DraIII (CACTGCTG); Site_2: DraIII (CACCTATG); 1st strand cDNA was primed with an oligo(dT) primer [ATGGTGGCCGTTTTTTTTTT]; double stranded cDNA was ligated to a DraIII adaptor [TGTGCGCTTCTGG], digested and cloned into distinct DraIII sites of the PME18S-FL3 vector (5' site CACTGCTG, 3' site CACCTATG). Klenow should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumi Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCCTGCTCAAAGCTGG and 3' end primer CGACCTGCGCTCAGCAGA."		
BASE COUNT	143 a 129 c 116 g 117 t		
ORIGIN			
Query Match	35.4%	Score 166.8; DB 8; length 505;	
Best Local Similarity	98.8%	Pred. No. 5.8e-35;	
Matches	168; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	1	AACTTGGCCGACTCTACTGTACACCGCAGTATCGGATAATGACCAAGTCTC	60
Db	336	AACTTGGCCGACTCTACTGTACACCGCAGTATCGGATAATGACCAAGTCTC	395
QY	61	TTCGTGACCAAAGACGCTCTGTTGAGGATATGACTGATATTGATCAAAGTGCAGT	120
	TTCGTGACCAAAGACGCTCTGTTGAGGATATGACTGATATTGATCAAAGTGCAGT	455	
Db	396		
QY	121	GAACCCGAGACGAGACTGATAATACATGATCAAAGACGAGCTGAAGTAA	170

Sat Nov 25 20:12:56 2000

us-09-373-230-1.rst

